



2023年第7期总382期

## 蔬菜育种专题

### 本期导读

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2023年2月13日

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## 学术文献

### 1. Comprehensive Volatilome Signature of Various Brassicaceae Species (不同芸苔科植物挥发性物的综合特征)

**简介:** To investigate in detail the volatilomes of various Brassicaceae species, landraces, and accessions, and to extract specific volatile markers, volatile aroma compounds were isolated from plant samples by headspace solid-phase microextraction and analyzed by gas chromatography/mass spectrometry (HS-SPME-GC/MS). The data obtained were subjected to uni- and multivariate statistical analysis. In general, two cabbage (*Brassica oleracea* L. var. capitata) landraces emitted the lowest amounts of volatiles generated in the lipoxygenase (LOX) pathway. Wild species *Brassica incana* Ten. and *Brassica mollis* Vis. were characterized by relatively high trans-2-hexenal/cis-3-hexen-1-ol ratio in relation to other investigated samples. A Savoy cabbage (*Brassica oleracea* L. var. sabauda) cultivar and three kale (*Brassica oleracea* L. var. acephala) accessions exhibited particular similarities in the composition of LOX volatiles, while the LOX volatilome fraction of *B. incana* and *B. mollis* partially coincided with that of another wild species, *Diplotaxis tenuifolia* L. Regarding volatiles formed in the glucosinolate (GSL) pathway, Savoy cabbage and wild species *B. incana*, *B. mollis*, and *D. tenuifolia* showed more intense emission of isothiocyanates than cabbage and kale. *Diplotaxis tenuifolia* showed a rather limited production of nitriles. The results of this study contribute to the general knowledge about volatile composition from various Brassicaceae species, which could be exploited for their better valorization. Future studies should focus on the influence of various environmental, cultivation, and post-harvest factors to obtain data with a higher level of applicability in practice.

**来源:** Plants

**发布日期:** 2023-01-01

**全文链接:**

[http://agri.ckcest.cn/file1/M00/10/1D/Csgk0GPjBTaAbo\\_JADF4eGrZ8nE078.pdf](http://agri.ckcest.cn/file1/M00/10/1D/Csgk0GPjBTaAbo_JADF4eGrZ8nE078.pdf)

### 2. Brassinosteroids fine-tune secondary and primary sulfur metabolism through BZR1-mediated transcriptional regulation (植物激素油菜素甾醇通过其信号转导组分bZR1精细调控初生硫代谢和次生硫代谢的分子机理)

**简介:** For adaptation to ever-changing environments, plants have evolved elaborate metabolic systems coupled to a regulatory network for optimal growth and defense. Regulation of plant secondary metabolic pathways such as glucosinolates (GSLs) by defense phytohormones in response to different stresses and nutrient deficiency has been intensively investigated, while how growth-promoting hormone balances plant secondary and primary metabolism has been largely unexplored. Here, we found that growth-promoting hormone brassinosteroid (BR) inhibits GSLs accumulation while enhancing biosynthesis of primary sulfur metabolites, including cysteine (Cys) and glutathione (GSH) both in *Arabidopsis* and Brassica crops, fine-tuning secondary and primary sulfur metabolism to promote plant growth. Furthermore,

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we demonstrate that of BRASSINAZOLE RESISTANT 1 (BZR1), the central component of BR signaling, exerts distinct tran-scriptional inhibition regulation on indolic and ali-phatic GSL via direct MYB51 dependent repression of indolic GSL bi-osynthesis, while exerting partial MYB29 dependent repression of aliphatic GSL biosynthesis. Additionally, BZR1 directly activates the transcription of APR1 and APR2 which encodes rate-limiting enzyme adenosine 5'-phosphosulfate reductases in the primary sulfur metabolic pathway. In summary, our findings indicate that BR inhibits the biosynthesis of GSLs to prioritize sulfur usage for primary metabolites under normal growth conditions. These findings expand our understanding of BR promoting plant growth from a metabolism per-spective.

来源: JIPB

发布日期:2022-12-27

全文链接:

<http://agri.ckcest.cn/file1/M00/03/4B/Csgk0Yg5uDaAFpLVAC7HxkVbgec275.pdf>

### **3. Profiling of Redox-Active Lipophilic Constituents in Leaf Mustard (*Brassica juncea* (L.) Czern.) Cultivars Using LC-MS and GC-MS (芥菜品种氧化还原活性亲脂性成分分析)**

简介: Leaf mustard is an important commercial and culinary vegetable. However, only limited information is available on the content and composition of the nutritionally important lipophilic constituents in these leaves. This research presents information on the contents and composition of carotenoids, tocopherols, phytosterols, and fatty acids in four cultivars of leaf mustard. The carotenoids and tocopherols were analyzed utilizing liquid chromatography (LC)-mass spectrometry (MS) with single ion monitoring (SIM), while phytosterols and fatty acids were analyzed using gas chromatography (GC)-MS and GC-flame ionization detection (FID), respectively. The LC-MS results revealed the dominance of (all-E)-lutein, within the range of 37.12 (cv. Asia Curled)-43.54% (cv. Jeok) of the total carotenoids. The highest amount of all of the individual carotenoids and total carotenoids (143.85  $\mu\text{g/g}$  fresh weight; FW) were recorded in cv. Cheong. Among the studied leaf samples, 67.16 (cv. Asia Curled)-83.42  $\mu\text{g/g}$  FW (cv. Cheong) of  $\alpha$ -tocopherol was recorded. Among the phytosterols,  $\beta$ -sitosterol was the most dominant one among the studied mustard leaves, accounting for 80.42 (cv. Jeok)-83.14% (cv. Red frill) of the total phytosterols. The fatty acid analysis revealed the presence of a significant amount of rare hexadecatrienoic acid (C16:3n3) in the studied mustard leaves, which accounted for 27.17 (cv. Asia Curled)-32.59% (cv. Red frill) of the total fatty acids. Overall, the cv. Cheong represented the highest contents of carotenoids, tocopherols, and phytosterols. Moreover, cv. Red frill contains the highest amount of n-3 PUFAs and antioxidant compounds. Thus, these cultivars can be promoted in cuisines which can be eaten to obtain the highest health benefits.

来源: Antioxidants

发布日期:2022-12-14

全文链接:

<http://agri.ckcest.cn/file1/M00/03/4B/Csgk0Yg5snGAOEDvADXjb000j0Y332.pdf>

#### **4. Transcriptome sequencing and analysis during seed growth and development in tomato (番茄种子生长发育过程中转录组的测序与分析)**

**简介:** Seed development is a complex process that includes the changes in seed size and the accumulation of various nutrients, and the process is regulated by many genes. Tomato is an important vegetable crop with extremely high nutritional value. Previous studies on tomato have focused mainly on fruit development and ripening, while few studies on the molecular mechanism of tomato seed development have been reported. In this study, we first compared the morphology of five stages of tomato seed development and measured the physiological changes of each stage. RNA-Seq showed that numerous differentially expressed genes (DEGs) were involved in seed development, including transcription factors (TFs), hormone biosynthesis and signal transduction, and starch biosynthesis-related genes. Of these genes, 54 DEGs were identified as the key candidate genes for tomato seed size by homologous query of known seed size-related genes in different plants. On this basis, 20 DEGs related to seed development were validated by quantitative real-time polymerase chain reaction (qRT-PCR), and the results showed high consistency with the RNA-Seq results. Finally, the yeast two-hybrid results showed that SIMBP3 interacts with three transcription factors, which may play important roles in tomato seed development. In short, our results analyzed in depth the gene expression profile of hormone-, transcription factor- and starch-related genes involved in tomato seed development. This study not only provides abundant genomic resources for seed development but also provides many references for future research on seed development and insights into the dynamics of gene regulation underlying seed development in tomato.

**来源:** Scientia Horticulturae

**发布日期:** 2022-12-13

**全文链接:**

[http://agri.ckcest.cn/file1/M00/10/1D/Csgk0GPi\\_zeAI2ZQAGdsRH6q90k842.pdf](http://agri.ckcest.cn/file1/M00/10/1D/Csgk0GPi_zeAI2ZQAGdsRH6q90k842.pdf)

#### **5. Safety evaluation of FAD2 RNAi transgenic Brassica napus L. based on microbial diversity and metabonomic analysis (基于微生物多样性和代谢组学分析的FAD2RNAi转基因甘蓝型油菜安全性评价)**

**简介:** Oleic acid desaturase (FAD2) is the key enzyme that produces polyunsaturated fatty acids in rapeseed (*Brassica napus* L), which is one of the main oil crops. RNA interference (RNAi) is an emerging technique that provides new opportunities for the generation of new traits in plants. To increase oleic acid content and reduce linoleic and linolenic acid content in rapeseed, we constructed an ihpRNA plant expression vector of the FAD2 gene and obtained transgenic plants for multiple generations by stable inheritance. In this study, third-generation transgenic plants (T3), seventh-generation transgenic plants (T7), and wild-type plants (WT) were used. The differences in microbial community diversity between transgenic plants and wild-type plants and the up- and downregulation of rhizosphere metabolite contents were investigated. In conclusion, the results showed that the soil microbial community structure was stable, the general microbial community structure was not changed by the transgenic

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rhizosphere exudates, and no significant harmful root exudate of transgenic rapeseed on the environment was found through the microbial community and metabolomics analysis. This work may provide an understanding of the impact of RNAi on plant metabolites and a safety evaluation method for transgenic plants and a reference for rapeseed breeding.

来源: Front Plant Sci

发布日期:2022-12-01

全文链接:

[http://agri.ckcest.cn/file1/M00/10/1D/Csgk0Gpi\\_VyAI0htAHGNY5fWdDU479.pdf](http://agri.ckcest.cn/file1/M00/10/1D/Csgk0Gpi_VyAI0htAHGNY5fWdDU479.pdf)